Proteomic insights into toxin diversity in Indian *Naja oxiana* venom and investigation of immunoreactivity profiles of two polyvalent antivenoms

Archana Deka^{1±*}, Robin Doley¹, Anita Malhotra²

¹Department of Molecular Biology and Biotechnology, Tezpur University, Assam-784028 ²Molecular Ecology and Evolution @ Bangor (MEEB), School of Natural Sciences, Bangor University, UK ±Current address: ICMR-Regional Medical Research Centre, N.E. Region, Assam, India *Email: archanadeka001@gmail.com

The venom proteomics of Indian *Naja oxiana* was characterized by SDS-PAGE, reverse-phase HPLC and mass spectrometry-based proteomics. The venom proteome of N. oxiana was found to be unique among other *Naja* species (*N. naja* and *N. kaouthia*). Three-finger toxins (85.3%) and snake venom metalloproteinase (9.1%) were the most dominant toxin families. Less abundant proteins included cardiotoxins, 5'-nucleotidases, cysteine rich secretory proteins, cobra venom factor, l-amino acid oxidase, phosphodiesterases. The immunoreactivity of two Indian polyvalent antivenoms (VINS and Premium Serums) was investigated by immunoblotting and immunoaffinity chromatography profiling. Immunoblotting analysis revealed that both antivenoms more effectively recognize higher molecular weight venom proteins than the lower mass. Further, immunological profiling of antivenoms revealed quantitative differences in immunorecognition capacity between the two antivenoms. The unbound proteins eluted from immunochromatography columns were characterized as non-immunodepleted toxins, and identified as three-finger toxins. These neglected toxins could limit antivenom efficacy in treating *N. oxiana* envenomings.

Keywords

Snake venom; Naja oxiana; Proteomics; Venom toxins; Three-finger toxins; Antivenomics